```
============================================================
Sequence Listing could not be accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: Tue Jul 17 13:54:26 EDT 2007
============================================================


*************************************************************
Reviewer Comments:


<210>    4
<211>    11
<212>    DNA
<213>    Artificial Sequence
<220>
<223>    Primer
<220>
<221>    misc_feature
<222>    (4)..(4)
<223>    a or g or c or t/u
<220>
<221>    misc_feature
<222>    (3)..(3)
<223>    a or g or c or t/u
<400>    4
ggncgcwbsg g                         11


The above <222> (4)..(4) and the <223> response under it are
incorrect:  "c," not "n," is at location 4, and can only represent itself.
*************************************************************
```

```
                 Validated By CRFValidator v 1.0.2

Application No:        10593357         Version No:        1.1


                 Input Set:


                 Output Set:



           Started:    2007-07-16 13:54:05.493
          Finished:    2007-07-16 13:54:08.628
           Elapsed:    0 hr(s) 0 min(s) 3 sec(s) 135 ms
    Total Warnings:    86
      Total Errors:    0
No. of SeqIDs Defined:  86
  Actual SeqID Count:   86
```

Error code   Error Description

```
W  213        Artificial or Unknown found in <213>  in SEQ ID (1)

W  213        Artificial or Unknown found in <213>  in SEQ ID (2)

W  213        Artificial or Unknown found in <213>  in SEQ ID (3)

W  213        Artificial or Unknown found in <213>  in SEQ ID (4)

W  213        Artificial or Unknown found in <213>  in SEQ ID (5)

W  213        Artificial or Unknown found in <213>  in SEQ ID (6)

W  213        Artificial or Unknown found in <213>  in SEQ ID (7)

W  213        Artificial or Unknown found in <213>  in SEQ ID (8)

W  213        Artificial or Unknown found in <213>  in SEQ ID (9)

W  213        Artificial or Unknown found in <213>  in SEQ ID (10)

W  213        Artificial or Unknown found in <213>  in SEQ ID (11)

W  213        Artificial or Unknown found in <213>  in SEQ ID (12)

W  213        Artificial or Unknown found in <213>  in SEQ ID (13)

W  213        Artificial or Unknown found in <213>  in SEQ ID (14)

W  213        Artificial or Unknown found in <213>  in SEQ ID (15)

W  213        Artificial or Unknown found in <213>  in SEQ ID (16)

W  213        Artificial or Unknown found in <213>  in SEQ ID (17)

W  213        Artificial or Unknown found in <213>  in SEQ ID (18)

W  213        Artificial or Unknown found in <213>  in SEQ ID (19)

W  213        Artificial or Unknown found in <213>  in SEQ ID (20)
```

Input Set:

Output Set:

Started:	2007-07-16 13:54:05.493
Finished:	2007-07-16 13:54:08.628
Elapsed:	0 hr(s) 0 min(s) 3 sec(s) 135 ms
Total Warnings:	86
Total Errors:	0
No. of SeqIDs Defined:	86
Actual SeqID Count:	86

Error code   Error Description

This error has occured more than 20 times, will not be displayed

<110>   BRAIN BIOTECHNOLOGY RESEARCH AND INFORMATION NETWORK AG

         Verseck, Stefan

         Liebeton, Klaus

         Eck, Jurgen

<120>   Nitrile hydratases from metagenome libraries

<130>   009848-0356700

<140>   10/593,357
<141>   2006-09-18

<150>   WO PCT/EP2005/002556
<151>   2005-03-10

<150>   DE 10 2004 013 842.7
<151>   2004-03-20

<160>   86

<170>   PatentIn version 3.1

<210>   1
<211>   12
<212>   DNA
<213>   Artificial Sequence
<220>
<223>   Primer

<400>   1
gcsmrsgcst gg   12

<210>   2
<211>   11
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Primer

<400>   2
ggsctsccsc c   11

<210>   3
<211>   11
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Primer

<400>   3
ggsggsagsc c   11

<210> 4
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (4)..(4)
<223> a or g or c or t/u

<220>
<221> misc_feature
<222> (3)..(3)
<223> a or g or c or t/u

<400> 4
ggncgcwbsg g   11

<210> 5
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (3)..(3)
<223> a or c

<220>
<221> misc_feature
<222> (9)..(9)
<223> a or g or c or t/u

<400> 5
gcnmrrgcnt gg   12

<210> 6
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (3)..(3)
<223> a or g or c or t/u

<220>
<221> misc_feature
<222> (6)..(6)
<223> a or g or c or t/u

<220>
<221> misc_feature
<222> (9)..(9)
<223> a or g or c or t/u

<400> 6
ggnytnccnc c   11

<210> 7
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (3)..(3)
<223> a or g or c or t/u

<220>
<221> misc_feature
<222> (6)..(6)
<223> a or g or c or t/u

<220>
<221> misc_feature
<222> (9)..(9)
<223> a or g or c or t/u

<400> 7
ggnggnarnc c   11

<210> 8
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (3)..(3)
<223> a or g or c or t/u

<400> 8
gwngwrtccc a   11

<210> 9
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (3)..(3)
<223> a or g or c or t/u

<220>
<221> misc_feature
<222> (9)..(9)
<223> a or g or c or t/u

<400> 9
gcntggryng a   11

<210> 10
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (3)..(3)
<223> a or g or c or t/u

<220>
<221> misc_feature
<222> (9)..(9)
<223> a or g or c or t/u

<400> 10

ggnytsccnc c   11

<210> 11
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (3)..(3)
<223> a or g or c or t/u

<220>
<221> misc_feature
<222> (9)..(9)
<223> a or g or c or t/u

<400> 11

ggnggsarnc c   11

<210> 12
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (3)..(3)
<223> a or g or c or t/u

<400> 12

swnswrtccc a   11

<210> 13
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 13

gccaaggtcg tc   12

<210> 14
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 14
ggccggtcct g   11

<210> 15
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 15
tccttgtacc aggtc   15

<210> 16
<211> 7
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
gcccgcc   7

<210> 17
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
ggcgctaaag ttgtt   15

<210> 18
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
tggccggttc tg   12

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
caaattcttt ataccaagtc   20

<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 20
ccatatatcg catttcagct   20

<210> 21
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
ggtcgtggcc aag   13

<210> 22
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
ggccggtcct g   11

<210> 23
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 23
tccttgtacc aggtc   15

<210> 24
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 24
gcgcatttcg gcg   13

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 25
gccaaggtcg tcgcsmrsgc stgg   24

<210> 26
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 26
ggccggtcct gggsctsccs cc   22

<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 27
tccttgtacc aggtcggsgg sagscc   26

<210> 28

<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (10)..(10)
<223> a or c or g or t/u

<400> 28
gcccgccggn cgcwbsgg   18

<210> 29
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (18)..(18)
<223> a or c or g or t/u

<220>
<221> misc_feature
<222> (24)..(24)
<223> a or c or g or t/u

<400> 29
ggcgctaaag ttgttgcnmr rgcntgg   27

<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (15)..(15)
<223> a or c or g or t/u

<220>
<221> misc_feature

<222> (18)..(18)
<223> a or c or g or t/u

<220>
<221> misc_feature
<222> (21)..(21)
<223> a or c or g or t/u

<400> 30
tggccggttc tgggnytncc nc   22

<210> 31
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (23)..(23)
<223> a or c or g or t/u

<220>
<221> misc_feature
<222> (26)..(26)
<223> a or c or g or t/u

<220>
<221> misc_feature
<222> (29)..(29)
<223> a or c or g or t/u

<400> 31
caaattcttt ataccaagtc ggnggnarnc c   31

<210> 32
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (23)..(23)
<223> a or c or g or t/u

<400> 32

ccatatatcg catttcagct gwngwrtccc a   31

<210> 33
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (16)..(16)
<223> a or c or g or t/u

<220>
<221> misc_feature
<222> (22)..(22)
<223> a or c or g or t/u

<400> 33

ggtcgtggcc aaggcntggr ynga   24

<210> 34
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (14)..(14)
<223> a or c or g or t/u

<220>
<221> misc_feature
<222> (20)..(20)
<223> a or c or g or t/u

<400> 34

ggccggtcct gggnytsccn cc   22

<210> 35
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (18)..(18)
<223> a or c or g or t/u

<220>
<221> misc_feature
<222> (24)..(24)
<223> a or c or g or t/u

<400> 35
tccttgtacc aggtcggngg sarncc   26

<210> 36
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (16)..(16)
<223> a or c or g or t/u

<400> 36
gcgcatttcg gcgswnswrt ccca   24

<210> 37
<211> 705
<212> DNA
<213> Unknown

<220>
<223> Metagenome - alpha unit nitrile hydratase - M6aH6

<220>
<221> CDS
<222> (1)..(705)

<400> 37

atg agc aag cac gta cac gat tac tac gcg aag aag aag cac gac cac   48
Met Ser Lys His Val His Asp Tyr Tyr Ala Lys Lys Lys His Asp His
1   5   10   15

```
gat cat gac cac gac gtc cac gag gcg atc gag gac cgg gac gag ggt          96
Asp His Asp His Asp Val His Glu Ala Ile Glu Asp Arg Asp Glu Gly
            20              25              30

ccg ccg tcg gaa ttc gag atc atg agc cgc gcc atg cag gag ctg ctg         144
Pro Pro Ser Glu Phe Glu Ile Met Ser Arg Ala Met Gln Glu Leu Leu
            35              40              45

gaa gag aag ggc gtc gtc acc gcg gag cag gtc cgg cgc agc atg gag         192
Glu Glu Lys Gly Val Val Thr Ala Glu Gln Val Arg Arg Ser Met Glu
            50              55              60

aag ttc gag gaa gag ctg ccc tac cgg ggg gcg cgg gtc gtc gcg cac         240
Lys Phe Glu Glu Glu Leu Pro Tyr Arg Gly Ala Arg Val Val Ala His
65              70              75              80

gcc tgg acc gac ccg gaa ttc aag aag cgg ctg ctg gcg gac ggc aag         288
Ala Trp Thr Asp Pro Glu Phe Lys Lys Arg Leu Leu Ala Asp Gly Lys
                85              90              95

gcc gcc gtc tcg gag ttc ggc atc gat ttg gaa gcc gag cgg ctg atc         336
Ala Ala Val Ser Glu Phe Gly Ile Asp Leu Glu Ala Glu Arg Leu Ile
            100             105             110

gcg gtc gcg aac aca acg gac gtg cac aac gtc atc gtg tgc acg ctg         384
Ala Val Ala Asn Thr Thr Asp Val His Asn Val Ile Val Cys Thr Leu
            115             120             125

tgc tcg tgc tac ccg cgc acg ctg ctc ggc atg ccg ccg acc tgg tac         432
Cys Ser Cys Tyr Pro Arg Thr Leu Leu Gly Met Pro Pro Thr Trp Tyr
    130             135             140

aag agc gat aac tac cgc tcg cgc gtg gtc tac gaa ccg cgc gcg gtg         480
Lys Ser Asp Asn Tyr Arg Ser Arg Val Val Tyr Glu Pro Arg Ala Val
145             150             155             160

ctg aag gaa ttc ggc acc gtg ctg ccg gag cgc gtc acc gtg cgc gtg         528
Leu Lys Glu Phe Gly Thr Val Leu Pro Glu Arg Val Thr Val Arg Val
                165             170             175

cac gac tcc aac gcc gac atg cgc tac gtg gtg atc ccc atg cgc ccg         576
His Asp Ser Asn Ala Asp Met Arg Tyr Val Val Ile Pro Met Arg Pro
            180             185             190

cag gga acc gag ggc tgg agc gag gag cgg ctc gcg gag ctg ctg acg         624
Gln Gly Thr Glu Gly Trp Ser Glu Glu Arg Leu Ala Glu Leu Leu Thr
            195             200             205

cgc gac acg ctg gtg ggg gtc acc gtg cca aaa gtg gaa gtc gga agt         672
Arg Asp Thr Leu Val Gly Val Thr Val Pro Lys Val Glu Val Gly Ser
            210             215             220

cga aag tcg aaa ggc gga agt aaa acc cgc tag                             705
Arg Lys Ser Lys Gly Gly Ser Lys Thr Arg
225             230
```

<210> 38
<211> 234
<212> PRT
<213> Unknown

<220>
<223> Metagenome – alpha unit nitrile hydratase – M6aH6

<400> 38

Met Ser Lys His Val His Asp Tyr Tyr Ala Lys Lys Lys His Asp His
1   5   10   15

Asp His Asp His Asp Val His Glu Ala Ile Glu Asp Arg Asp Glu Gly
                20   25   30

Pro Pro Ser Glu Phe Glu Ile Met Ser Arg Ala Met Gln Glu Leu Leu
                35   40   45

Glu Glu Lys Gly Val Val Thr Ala Glu Gln Val Arg Arg Ser Met Glu
            50   55   60

Lys Phe Glu Glu Glu Leu Pro Tyr Arg Gly Ala Arg Val Val Ala His
65   70   75   80

Ala Trp Thr Asp Pro Glu Phe Lys Lys Arg Leu Leu Ala Asp Gly Lys
                85   90   95

Ala Ala Val Ser Glu Phe Gly Ile Asp Leu Glu Ala Glu Arg Leu Ile
                100   105   110

Ala Val Ala Asn Thr Thr Asp Val His Asn Val Ile Val Cys Thr Leu
                115   120   125

Cys Ser Cys Tyr Pro Arg Thr Leu Leu Gly Met Pro Pro Thr Trp Tyr
            130   135   140

Lys Ser Asp Asn Tyr Arg Ser Arg Val Val Tyr Glu Pro Arg Ala Val
145   150   155   160

Leu Lys Glu Phe Gly Thr Val Leu Pro Glu Arg Val Thr Val Arg Val
                165   170   175

His Asp Ser Asn Ala Asp Met Arg Tyr Val Val Ile Pro Met Arg Pro
                180   185   190

```
Gln Gly Thr Glu Gly Trp Ser Glu Glu Arg Leu Ala Glu Leu Leu Thr
        195                 200                 205


Arg Asp Thr Leu Val Gly Val Thr Val Pro Lys Val Glu Val Gly Ser
        210                 215                 220


Arg Lys Ser Lys Gly Gly Ser Lys Thr Arg
225                 230



<210>   39
<211>   657
<212>   DNA
<213>   Unknown

<220>
<223>   Metagenome - alpha unit nitrile hydratase - M12K24

<220>
<221>   CDS
<222>   (1)..(657)



<400>   39


atg tcg gac gga aca aca att gga atc cag gcc gcg aca acc ctt cga     48
Met Ser Asp Gly Thr Thr Ile Gly Ile Gln Ala Ala Thr Thr Leu Arg
1               5                   10                  15


tca gcc atg aac att cca gct cgt gaa ttc gcc ctc cag cgc act gcg     96
Ser Ala Met Asn Ile Pro Ala Arg Glu Phe Ala Leu Gln Arg Thr Ala
                20                  25                  30


ccg gtc gag cag cgt gtc gac gcg atc cag gcg gcg ctc gac gaa cgc    144
Pro Val Glu Gln Arg Val Asp Ala Ile Gln Ala Ala Leu Asp Glu Arg
        35                  40                  45


ggt ttg aac gcc agt gac gca gtc cag gaa ttg agc cac ctg gcg gag    192
Gly Leu Asn Ala Ser Asp Ala Val Gln Glu Leu Ser His Leu Ala Glu
    50                  55                  60


gag caa tgg att ccg cgc aat ggc gcg cgg gtc gtc gcc aaa gcc tgg    240
Glu Gln Trp Ile Pro Arg Asn Gly Ala Arg Val Val Ala Lys Ala Trp
65                  70                  75                  80


gtc gac ccg gaa ttc cgc gcg cgg ctt ctg gcc gac ggt cgc gcc gcc    288
Val Asp Pro Glu Phe Arg Ala Arg Leu Leu Ala Asp Gly Arg Ala Ala
                85                  90                  95


gtt gcc gaa ctg ggc ctc tcg atg ccg aag cat cac cgg cac ctc gtg    336
Val Ala Glu Leu Gly Leu Ser Met Pro Lys His His Arg His Leu Val
            100                 105                 110


gtg ctg gag aac acg ccg agc gtg cag aac gtc atc tgc tgc acg cag    384
```

```
Val Leu Glu Asn Thr Pro Ser Val Gln Asn Val Ile Cys Cys Thr Gln
        115                 120                 125


tgc tcg tgc acg gcg ttc acg atc atc gga ctg ccg ccc gac tgg tac        432
Cys Ser Cys Thr Ala Phe Thr Ile Ile Gly Leu Pro Pro Asp Trp Tyr
        130                 135                 140


aag gac ctg gaa tac cgc gcg cga gtc gtc cgg gag tcg cgc acc gtg        480
Lys Asp Leu Glu Tyr Arg Ala Arg Val Val Arg Glu Ser Arg Thr Val
145                 150                 155                 160


ctg aag gag atg gga ctg gat ctg cct cgg gat gtc gaa att cgc gtc        528
Leu Lys Glu Met Gly Leu Asp Leu Pro Arg Asp Val Glu Ile Arg Val
                    165                 170                 175


tgg gat acc act gcc gac acg cgc tac atg gta ttg ccg gta cag ccg        57
```